RAW SEQUENCE LISTING   DATE: 10/07/2003
PATENT APPLICATION: **US/08/913,644**   TIME: 13:59:02

Input Set : **A:\19424PC Seq List.txt**
Output Set: **N:\CRF4\10072003\H913644.raw**

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 4 <110> APPLICANT: Hofmann, Kathryn J.
 5        Jansen, Kathrin U.
 6        Neeper, Michael P.
 8 <120> TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE
 9        18
11 <130> FILE REFERENCE: 19424PC
13 <140> CURRENT APPLICATION NUMBER: 08/913,644
14 <141> CURRENT FILING DATE: 1997-11-21
16 <150> PRIOR APPLICATION NUMBER: PCT/US96/03649
17 <151> PRIOR FILING DATE: 1996-03-18
19 <150> PRIOR APPLICATION NUMBER: 08/408,669
20 <151> PRIOR FILING DATE: 1995-03-22
22 <150> PRIOR APPLICATION NUMBER: 08/409,122
23 <151> PRIOR FILING DATE: 1995-03-22
25 <160> NUMBER OF SEQ ID NOS: 16
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1524
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: HPV18 L1 Consensus Sequence
37 <400> SEQUENCE: 1
38 atggctttgt ggcggcctag tgacaatacc gtataccttc cacctccttc tgtggcaaga 60
39 gttgtaaata ctgatgatta tgtgactcgc acaagcatat tttatcatgc tggcagctct 120
40 agattattaa ctgttggtaa tccatatttt agggttcctg caggtggtgg caataagcag 180
41 gatattccta aggtttctgc ataccaatat agagtatttc gggtgcagtt acctgaccca 240
42 aataaatttg gtttacctga atatagtatt tataatcctg aaacacaacg tttagtgtgg 300
43 gcctgtgctg gagtggaaat tggccgtggt cagcctttag gtgttggcct tagtgggcat 360
44 ccattttata ataaattaga tgacactgaa agttcccatg ccgctacgtc taatgtttct 420
45 gaggacgtta gggacaatgt gtctgtagat tataagcaga cacagttatg tattttgggc 480
46 tgtgcccctg ctattgggga cactgggct aaaggcactg cttgtaaatc gcgtccttta 540
47 tcacagggcg attgccccc tttagaactt aagaacacag ttttggaaga tggtgatatg 600
48 gtagatactg gatatggtgc catggacttt agtacattgc aagatactaa atgtgaggta 660
49 ccattggata tttgtcagtc tatttgtaaa tatcctgatt atttacaaat gtctgcagat 720
50 ccttatgggg attccatgtt tttttgctta cgacgtgagc agcttttttgc taggcatttt 780
51 tggaataggg caggtactat gggtgacact gtgcctcaat ccttatatat taaaggcaca 840
52 ggtatgcgtg cttcacctgg cagctgtgtg tattctccct ctccaagtgg ctctattgtt 900
53 acctctgact cccagttgtt taataaacca tattggttac ataaggcaca gggtcataac 960
54 aatggtatct gctggcataa tcaattattt gttactgtgg tagataccac tcgtagtacc 1020
55 aatttaacaa tatgtgcttc tacacagtct cctgtacctg gcaatatga tgctaccaaa 1080
56 tttaagcagt atagcagaca tgttgaagaa tatgatttgc agtttatttt tcagttatgt 1140
57 actattactt taactgcaga tgttatgtcc tatattcata gtatgaatag cagtatttta 1200
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Input Set : **A:\19424PC Seq List.txt**
Output Set: **N:\CRF4\10072003\H913644.raw**

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58 gaggattgga actttggtgt tcccccccccg ccaactacta gtttggtgga tacatatcgt 1260
59 tttgtacaat ctgttgctat tacctgtcaa aaggatgctg caccagctga aaataaggat 1320
60 ccctatgata agttaaagtt ttggaatgtg gatttaaagg aaaagttttc tttggactta 1380
61 gatcaatatc cccttggacg taaatttttg gttcaggctg gattgcgtcg caagcccacc 1440
62 ataggccctc gtaaacgttc tgctccatct gccactacgt cttctaaacc tgccaagcgt 1500
63 gtgcgtgtac gtgccaggaa gtaa                                       1524
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 507
67 <212> TYPE: PRT
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:
71 <223> OTHER INFORMATION: HPV18 L1 Consensus Sequence
73 <400> SEQUENCE: 2
74 Met Ala Leu Trp Arg Pro Ser Asp Asn Thr Val Tyr Leu Pro Pro Pro
75 1               5                   10                  15
76 Ser Val Ala Arg Val Val Asn Thr Asp Asp Tyr Val Thr Arg Thr Ser
77            20                  25                  30
78 Ile Phe Tyr His Ala Gly Ser Ser Arg Leu Leu Thr Val Gly Asn Pro
79         35                  40                  45
80 Tyr Phe Arg Val Pro Ala Gly Gly Gly Asn Lys Gln Asp Ile Pro Lys
81      50                  55                  60
82 Val Ser Ala Tyr Gln Tyr Arg Val Phe Arg Val Gln Leu Pro Asp Pro
83 65                  70                  75                  80
84 Asn Lys Phe Gly Leu Pro Asp Asn Ser Ile Tyr Asn Pro Glu Thr Gln
85                 85                  90                  95
86 Arg Leu Val Trp Ala Cys Ala Gly Val Glu Ile Gly Arg Gly Gln Pro
87             100                 105                 110
88 Leu Gly Val Gly Leu Ser Gly His Pro Phe Tyr Asn Lys Leu Asp Asp
89         115                 120                 125
90 Thr Glu Ser Ser His Ala Ala Thr Ser Asn Val Ser Glu Asp Val Arg
91      130                 135                 140
92 Asp Asn Val Ser Val Asp Tyr Lys Gln Thr Gln Leu Cys Ile Leu Gly
93 145                 150                 155                 160
94 Cys Ala Pro Ala Ile Gly Glu His Trp Ala Lys Gly Thr Ala Cys Lys
95             165                 170                 175
96 Ser Arg Pro Leu Ser Gln Gly Asp Cys Pro Pro Leu Glu Leu Lys Asn
97             180                 185                 190
98 Thr Val Leu Glu Asp Gly Asp Met Val Asp Thr Gly Tyr Gly Ala Met
99         195                 200                 205
100 Asp Phe Ser Thr Leu Gln Asp Thr Lys Cys Glu Val Pro Leu Asp Ile
101     210                 215                 220
102 Cys Gln Ser Ile Cys Lys Tyr Pro Asp Tyr Leu Gln Met Ser Ala Asp
103 225                 230                 235                 240
104 Pro Tyr Gly Asp Ser Met Phe Phe Cys Leu Arg Arg Glu Gln Leu Phe
105             245                 250                 255
106 Ala Arg His Phe Trp Asn Arg Ala Gly Thr Met Gly Asp Thr Val Pro
107             260                 265                 270
108 Gln Ser Leu Tyr Ile Lys Gly Thr Gly Met Arg Ala Ser Pro Gly Ser
109             275                 280                 285
```

```
110 Cys Val Tyr Ser Pro Ser Pro Ser Gly Ser Ile Val Thr Ser Asp Ser
111     290             295             300
112 Gln Leu Phe Asn Lys Pro Tyr Trp Leu His Lys Ala Gln Gly His Asn
113 305             310             315             320
114 Asn Gly Ile Cys Trp His Asn Gln Leu Phe Val Thr Val Val Asp Thr
115             325             330             335
116 Thr Arg Ser Thr Asn Leu Thr Ile Cys Ala Ser Thr Gln Ser Pro Val
117         340             345             350
118 Pro Gly Gln Tyr Asp Ala Thr Lys Phe Lys Gln Tyr Ser Arg His Val
119         355             360             365
120 Glu Glu Tyr Asp Leu Gln Phe Ile Phe Gln Leu Cys Thr Ile Thr Leu
121     370             375             380
122 Thr Ala Asp Val Met Ser Tyr Ile His Ser Met Asn Ser Ser Ile Leu
123 385             390             395             400
124 Glu Asp Trp Asn Phe Gly Val Pro Pro Pro Thr Thr Ser Leu Val
125             405             410             415
126 Asp Thr Tyr Arg Phe Val Gln Ser Val Ala Ile Thr Cys Gln Lys Asp
127         420             425             430
128 Ala Ala Pro Ala Glu Asn Lys Asp Pro Tyr Asp Lys Leu Lys Phe Trp
129         435             440             445
130 Asn Val Asp Leu Lys Glu Lys Phe Ser Leu Asp Leu Asp Gln Tyr Pro
131     450             455             460
132 Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg Lys Pro Thr
133 465             470             475             480
134 Ile Gly Pro Arg Lys Arg Ser Ala Pro Ser Ala Thr Thr Ser Ser Lys
135             485             490             495
136 Pro Ala Lys Arg Val Arg Val Arg Ala Arg Lys
137         500             505
140 <210> SEQ ID NO: 3
141 <211> LENGTH: 1389
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: HPV18 L2 Consensus Sequence
148 <400> SEQUENCE: 3
149 atggtatccc accgtgccgc acgacgcaaa cgggcttcgg tgactgactt atataaaaca 60
150 tgtaaacaat ctggtacatg tccatctgat gttgttaata aggtagaggg caccacgtta 120
151 gcagataaaa tattgcaatg gtcaagcctt ggtatatttt gggtggact tggcataggt 180
152 actggaagtg gtacaggggg tcgtacaggg tacattccat gggtgggcg ttccaataca 240
153 gttgtggatg tcggtcctac acgtcctcca gtggttattg aacctgtggg ccccacagac 300
154 ccatctattg ttacattaat agaggactca agtgttgtta catcaggtgc acctaggcct 360
155 actttttactg gcacgtctgg gtttgatata acatctgctg gtacaactac acctgcagtt 420
156 ttggatatca caccttcgtc tacctctgtt tctatttcca caaccaattt taccaatcct 480
157 gcattttctg atccgtccat tattgaagtt ccacaaactg gggaggtgtc aggtaatgta 540
158 tttgttggta cccctacatc tggaacacat gggtatgaag aaataccttt acaaacattt 600
159 gcttcttctg gtacggggga ggaacccat agtagtaccc cattgcctac tgtgcggcgt 660
160 gtagcaggtc cccgccttta cagtagggcc taccaacaag tgtctgtggc taaccctgag 720
161 tttcttacac gtccatcctc tttaattacc tatgacaacc cggcctttga gcctgtggac 780
162 actacattaa catttgagcc tcgtagtaat gttcctgatt cagattttat ggatattatc 840
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/08/913,644**

DATE: 10/07/2003
TIME: 13:59:02

Input Set : **A:\19424PC Seq List.txt**
Output Set: **N:\CRF4\10072003\H913644.raw**

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163 cgtttacata ggcctgcttt aacatccagg cgtggtactg tgcgctttag tagattaggt 900
164 caaagggcaa ctatgtttac ccgtagcggt acacaaatag gtgctaggg tcacttttat 960
165 catgatataa gtcctattgc accctcccca gaatatattg aactgcagcc tttagtatct 1020
166 gccacggagg acaatggctt gtttgatata tatgcagatg acatagaccc tgcaatgcct 1080
167 gtaccatcgc gtcctactac ctcctctgca gtttctacat attcgcccac tatatcatct 1140
168 gcctcttcct atagtaatgt aacggtccct ttaacctcct cttgggatgt gcctgtatac 1200
169 acgggtcctg atattacatt accacctact acctctgtat ggcccattgt atcacccaca 1260
170 gcccctgcct ctacacagta tattggtata catggtacac attattattt gtggccatta 1320
171 tattatttta ttcctaaaaa gcgtaaacgt gttccctatt tttttgcaga tggctttgtg 1380
172 gcggcctag                                                          1389
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 461
176 <212> TYPE: PRT
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: HPV18 L2 Consensus Sequence
182 <400> SEQUENCE: 4
183 Met Val Ser His Arg Ala Ala Arg Arg Lys Arg Ala Ser Val Thr Asp
184   1               5                  10                  15
185 Leu Tyr Lys Thr Cys Lys Gln Ser Gly Thr Cys Pro Ser Asp Val Val
186              20                  25                  30
187 Asn Lys Val Glu Gly Thr Thr Leu Ala Asp Lys Ile Leu Gln Trp Ser
188          35                  40                  45
189 Ser Leu Gly Ile Phe Leu Gly Gly Leu Gly Ile Gly Thr Gly Ser Gly
190      50                  55                  60
191 Thr Gly Gly Arg Thr Gly Tyr Ile Pro Leu Gly Gly Arg Ser Asn Thr
192 65                  70                  75                  80
193 Val Val Asp Val Gly Pro Thr Arg Pro Pro Val Val Ile Glu Pro Val
194              85                  90                  95
195 Gly Pro Thr Asp Pro Ser Ile Val Thr Leu Ile Glu Asp Ser Ser Val
196              100                 105                 110
197 Val Thr Ser Gly Ala Pro Arg Pro Thr Phe Thr Gly Thr Ser Gly Phe
198          115                 120                 125
199 Asp Ile Thr Ser Ala Gly Thr Thr Thr Pro Ala Val Leu Asp Ile Thr
200      130                 135                 140
201 Pro Ser Ser Thr Ser Val Ser Ile Ser Thr Thr Asn Phe Thr Asn Pro
202 145                 150                 155                 160
203 Ala Phe Ser Asp Pro Ser Ile Ile Glu Val Pro Gln Thr Gly Glu Val
204              165                 170                 175
205 Ser Gly Asn Val Phe Val Gly Thr Pro Thr Ser Gly Thr His Gly Tyr
206              180                 185                 190
207 Glu Glu Ile Pro Leu Gln Thr Phe Ala Ser Ser Gly Thr Gly Glu Glu
208          195                 200                 205
209 Pro Ile Ser Ser Thr Pro Leu Pro Thr Val Arg Arg Val Ala Gly Pro
210      210                 215                 220
211 Arg Leu Tyr Ser Arg Ala Tyr Gln Gln Val Ser Val Ala Asn Pro Glu
212 225                 230                 235                 240
213 Phe Leu Thr Arg Pro Ser Ser Leu Ile Thr Tyr Asp Asn Pro Ala Phe
214              245                 250                 255
```

RAW SEQUENCE LISTING   DATE: 10/07/2003
PATENT APPLICATION: **US/08/913,644**   TIME: 13:59:02

Input Set : **A:\19424PC Seq List.txt**
Output Set: **N:\CRF4\10072003\H913644.raw**

```
215 Glu Pro Val Asp Thr Thr Leu Thr Phe Glu Pro Arg Ser Asn Val Pro
216             260             265             270
217 Asp Ser Asp Phe Met Asp Ile Ile Arg Leu His Arg Pro Ala Leu Thr
218         275             280             285
219 Ser Arg Arg Gly Thr Val Arg Phe Ser Arg Leu Gly Gln Arg Ala Thr
220     290             295             300
221 Met Phe Thr Arg Ser Gly Thr Gln Ile Gly Ala Arg Val His Phe Tyr
222 305             310             315             320
223 His Asp Ile Ser Pro Ile Ala Pro Ser Pro Glu Tyr Ile Glu Leu Gln
224             325             330             335
225 Pro Leu Val Ser Ala Thr Glu Asp Asn Gly Leu Phe Asp Ile Tyr Ala
226         340             345             350
227 Asp Asp Ile Asp Pro Ala Met Pro Val Pro Ser Arg Pro Thr Thr Ser
228         355             360             365
229 Ser Ala Val Ser Thr Tyr Ser Pro Thr Ile Ser Ser Ala Ser Ser Tyr
230     370             375             380
231 Ser Asn Val Thr Val Pro Leu Thr Ser Ser Trp Asp Val Pro Val Tyr
232 385             390             395             400
233 Thr Gly Pro Asp Ile Thr Leu Pro Pro Thr Ser Val Trp Pro Ile Val
234             405             410             415
235 Ser Pro Thr Ala Pro Ala Ser Thr Gln Tyr Ile Gly Ile His Gly Thr
236             420             425             430
237 His Tyr Tyr Leu Trp Pro Leu Tyr Tyr Phe Ile Pro Lys Lys Arg Lys
238         435             440             445
239 Arg Val Pro Tyr Phe Phe Ala Asp Gly Phe Val Ala Ala
240     450             455             460
243 <210> SEQ ID NO: 5
244 <211> LENGTH: 41
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: oligonucleotide, sense primer
251 <400> SEQUENCE: 5
252 gaagatctca caaaacaaaa tggctttgtg gcggcctagt g              41
254 <210> SEQ ID NO: 6
255 <211> LENGTH: 36
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: oligonucleotide, antisense primer
262 <400> SEQUENCE: 6
263 gaagatcttt acttcctggc acgtacacgc acacgc                    36
265 <210> SEQ ID NO: 7
266 <211> LENGTH: 45
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: oligonucleotide, sense primer
273 <400> SEQUENCE: 7
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VERIFICATION SUMMARY
DATE: 10/07/2003
PATENT APPLICATION: **US/08/913,644**
TIME: 13:59:03

Input Set : **A:\19424PC Seq List.txt**
Output Set: **N:\CRF4\10072003\H913644.raw**

4 M:271 C: Current Filing Date differs, Replaced Current Filing Date